AMENDMENT(S) TO THE SPECIFICATION

Please replace the paragraph running from the middle of p. 60 to the bottom of p. 61 of the application as filed (i.e., paragraph [0110] of the published application No. 2007/0196378 dated August 23, 2007), with the following rewritten paragraph:

The data obtained show that a number of open laser frames not characterized up to now are repressed by Rim101p, to which *RBR1* (orf6.6747), *RBR2* (orf6.6744) and *RBR3* (orf6.1159) belong. For the confirmation of the microarray data and for the quantification of the transcription of these genes, a Northern blot analysis was carried out. The results are shown in figure 1b. *RBR1, RBR2* and *RBR1* were acid-expressed, no significant expression in the wild-type being detected at a neutral pH. The *RBR* genes were repressed by dominantly active *RIM101-1426* at an acidic pH and strongly highly regulated under all conditions in Δ*rim101* mutant strains (see figures 1b and figure 4). According to an in silico investigation, all three *RIM101*-repressed genes have an N-terminal signal sequence comprising approximately 20 amino acid for transport into the endoplasmic reticulum and a C-terminal hydrophobic transmembrane domain. All RBR protein sequences likewise comprise a hydrophobic N-terminal domain. The transmembrane domains are characteristic of GPI-anchored cell wall proteins. To the transmembrane domains is connected a sequence situated upstream having an omega site, which defines the cleavage site for the addition of the GPI anchor as well as further determinants which define the location either in the cell wall or in the plasma membrane (Caro et al., Yeast, 13 (1997), 1477-1489; De Groot et al., Yeast, 20 (2003), 781-796; Frieman and Cormack, Mol. Microbiol., 50 (2003), 883-896). The proteins Rbr1p (111 amino acids) and Rbr2p (168 amino acids) have potential cleavage sites in positions 81 and 143 respectively. The protein Rbr3p (560 amino acids) shows a potential cleavage site in position 540. Moreover, the protein sequence, with the exception of the C- and N-terminal hydrophobic sequences, shows a number of sites having a high O-beta-glycosylation potential, which is typical for fungal cell wall proteins ~~(http://www.cbs.dtu.dk/services/YinOYang)~~ (see, for example, the internet web-site for the Center

for Biological Sequence Analysis (CBS) at the Technical University of Denmark, which cites to a publication, i.e., Gupta, R. and Brunak, S., "Prediction of glycosylation across the human proteome and the correlation to protein function,*Pacific Symposium on Biocomputing*,7: 310-322 (2002) setting forth the results obtained with the use of the YinOYang prediction server).

Please replace the paragraph at the top of p. 62 of the application as filed (i.e., paragraph [0111] of the published application No. 2007/0196378 dated August 23, 2007) with the following rewritten paragraph:

A search of pro- and eukaryotic genome databases at the National Center for Biotechnology Information ~~(http:// www.ncbi.nlm.nih.gov/BLAST)~~ (see, for example, the publication, Altschul, S.F., Gish, W., Miller, W., Myers, E.W., and Lipman, D.J., "Basic Local Alignment Search Tool". *J Mol. Biol.*, 215: 404-410 (1990) which contains the information referred to in the National Center for Biotechnology Information databases) showed that the RBR genes according to the invention show no significant homology to genes of *S. cerevisiae* or other organisms. It was seen that Rbr1p is approximately 40% identical with Hyr1p of *C. albicans*, a GPI-anchored, nonessential cell wall protein which very often occurs in hyphae (Bailey et al., J. Bacteriol., 178 (1996), 5353-5360).